





Per tile sequence quality

Per sequence quality scores

Per base sequence content

Per sequence GC content

Per base N content

Sequence Length Distribution

Sequence Duplication Levels

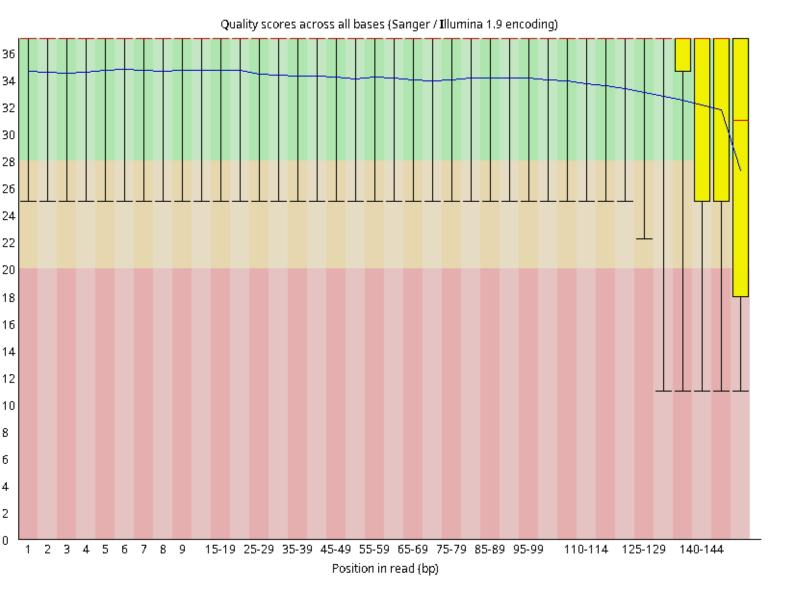
Overrepresented sequences

Adapter Content

Basic Statistics

Measure	Value	
Filename	SRR33784444_2.fastq	
File type	Conventional base calls	
Encoding	Sanger / Illumina 1.9	
Total Sequences	122837	
Sequences flagged as poor quality	0	
Sequence length	151	
%GC	46	

Per base sequence quality



Per tile sequence quality

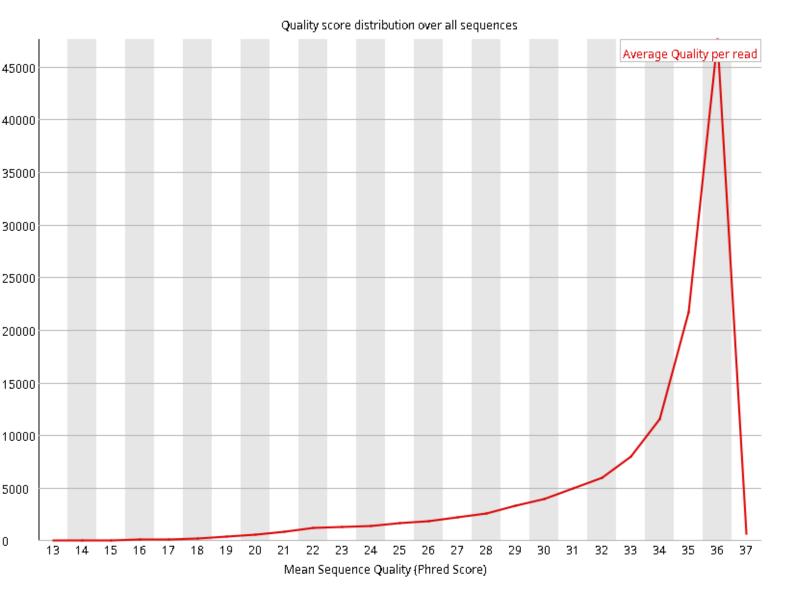
1102

1101

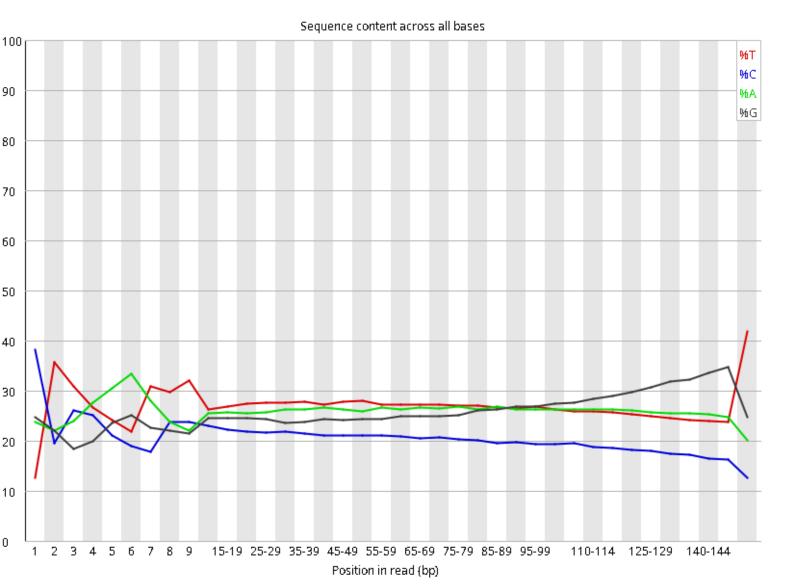


1 2 3 4 5 6 7 8 9 15-19 25-29 35-39 45-49 55-59 65-69 75-79 85-89 95-99 110-114 125-129 140-144 Position in read (bp)

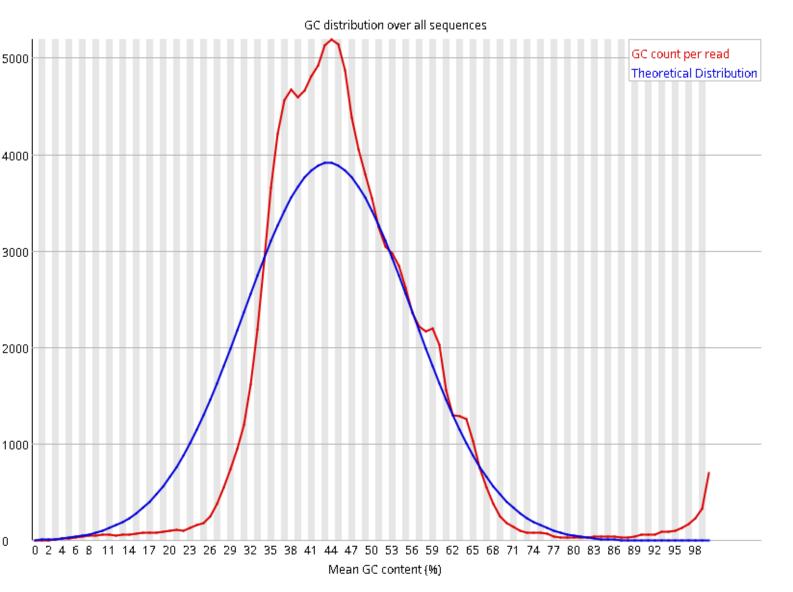
Per sequence quality scores



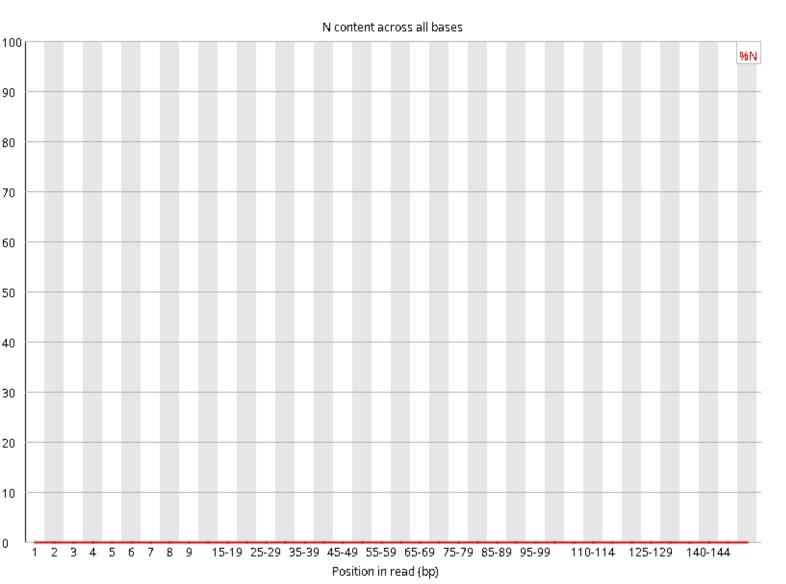
Per base sequence content



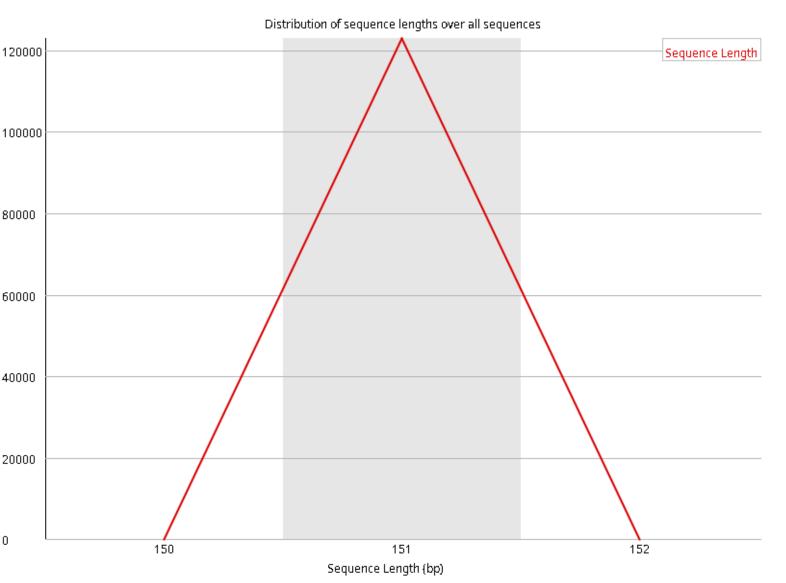
Per sequence GC content



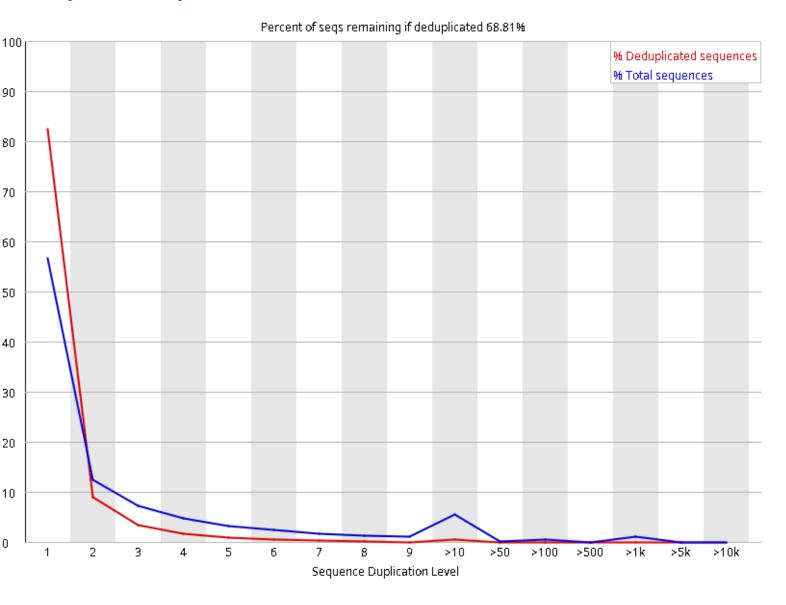




Sequence Length Distribution



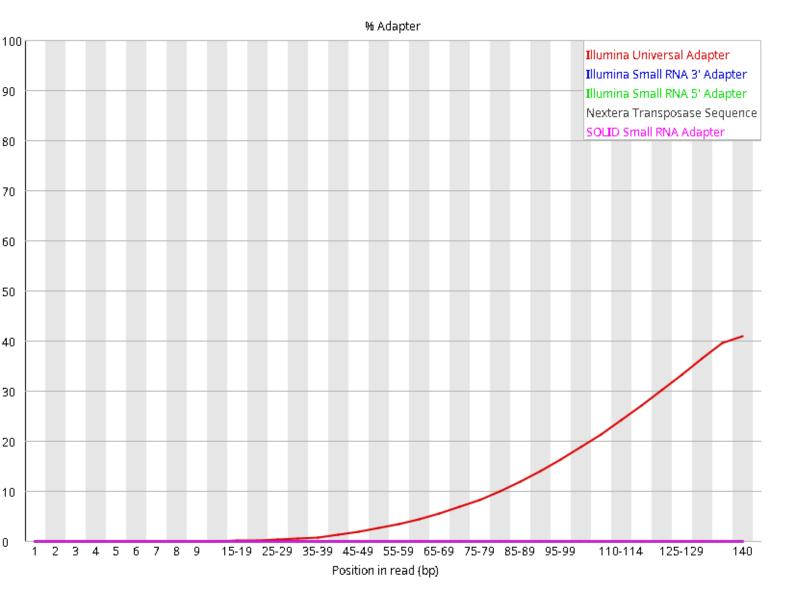
Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1647	1.340801224386789	No Hit
CCTCCAATTCCCCCTATCATTTTTGGTTTCCATTTTCCTGGTAAATTTAT	197	0.16037513127152242	No Hit
CCTCCAATTCCTCCTATCATTTTTGGTTTCCATTTTCCTGGTAAATTTAT	180	0.1465356529384469	No Hit
GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	155	0.12618347891921816	No Hit
CTCCAATTCCCCCTATCATTTTTGGTTTCCATTTTCCTGGTAAATTTATT	128	0.1042031309784511	No Hit

aAdapter Content



Produced by FastQC (version 0.11.7)